

SEQUENCE LISTING

<110> Kinch, Michael S.

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<151> 2003-12-24

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<170> PatentIn version 3.2

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Trp Thr Pro Pro Gln Asp Ser Gly Gly Arg Glu Asp Ile Val Tyr Ser	
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Val Thr Cys Glu Gln Cys Trp Pro Glu Ser Gly Glu Cys Gly Pro Cys	
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Ser Val Thr Val Ser Asp Leu Glu Pro His Met Asn Tyr Thr Phe Thr	
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Val Glu Ala Arg Asn Gly Val Ser Gly Leu Val Thr Ser Arg Ser Phe	
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Arg Thr Ala Ser Val Ser Ile Asn Gln Thr Glu Pro Pro Lys Val Arg	
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Val Thr Leu Asp Asp Leu Ala Pro Asp Thr Thr Tyr Leu Val Gln Val	
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Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala Gly Ser Lys Val His Glu	
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Phe Gln Thr Leu Ser Pro Glu Gly Ser Gly Asn Leu Ala Val Ile Gly	
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Tyr Met Tyr Ser Val Cys Asn Val Met Ser Gly Asp Gln Asp Asn Trp
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Leu Arg Thr Asn Trp Val Tyr Arg Gly Glu Ala Glu Arg Ile Phe Ile
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Arg Val Trp Lys Tyr Glu Val Thr Tyr Arg Lys Lys Gly Asp Ser Asn
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Ser Tyr Asn Val Arg Arg Thr Glu Gly Phe Ser Val Thr Leu Asp Asp
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Leu Ala Pro Asp Thr Thr Tyr Leu Val Gln Val Gln Ala Leu Thr Gln
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Glu Gly Gln Gly Ala Gly Ser Lys Val His Glu Phe Gln Thr Leu Ser
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Pro Glu Gly Ser Gly Asn Leu Ala Val Ile Gly Gly Val Ala Val Gly
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Val Val Leu Leu Leu Val Leu Ala Gly Val Gly Phe Phe Ile His Arg
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Arg Arg Lys Asn Gln Arg Ala Arg Gln Ser Pro Glu Asp Val Tyr Phe
 565 570 575

Ser Lys Ser Glu Gln Leu Lys Pro Leu Lys Thr Tyr Val Asp Pro His
 580 585 590

Thr Tyr Glu Asp Pro Asn Gln Ala Val Leu Lys Phe Thr Thr Glu Ile
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His Pro Ser Cys Val Thr Arg Gln Lys Val Ile Gly Ala Gly Glu Phe
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Gly Glu Val Tyr Lys Gly Met Leu Lys Thr Ser Ser Gly Lys Lys Glu
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His Asn Ile Ile Arg Leu Glu Gly Val Ile Ser Lys Tyr Lys Pro Met
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Arg Gly Ile Ala Ala Gly Met Lys Tyr Leu Ala Asn Met Asn Tyr Val
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His Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val
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Cys Lys Val Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro
755 760 765

Glu Ala Thr Tyr Thr Thr Ser Gly Gly Lys Ile Pro Ile Arg Trp Thr
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Pro Tyr Trp Glu Leu Ser Asn His Glu Val Met Lys Ala Ile Asn Asp
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Leu Lys Thr Leu Ala Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro
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Lys Arg Ile Gly Val Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr
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<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted fusion protein

<400> 20

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
20 25 30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser
35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Leu Glu Leu Gln Ala
50 55 60

Ala Arg Ala Cys Phe Ala Leu Leu Trp Gly Cys Ala Leu Ala Ala Ala
65 70 75 80

Ala Ala Ala Gln Gly Lys Glu Val Val Leu Leu Asp Phe Ala Ala Ala
85 90 95

Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr Gly Lys Gly Trp Asp
100 105 110

Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile Tyr Met Tyr Ser Val
115 120 125

Cys Asn Val Met Ser Gly Asp Gln Asp Asn Trp Leu Arg Thr Asn Trp
130 135 140

Val Tyr Arg Gly Glu Ala Glu Arg Ile Phe Ile Glu Leu Lys Phe Thr
145 150 155 160

Val Arg Asp Cys Asn Ser Phe Pro Gly Gly Ala Ser Ser Cys Lys Glu
165 170 175

Thr Phe Asn Leu Tyr Tyr Ala Glu Ser Asp Leu Asp Tyr Gly Thr Asn
 180 185 190

Phe Gln Lys Arg Leu Phe Thr Lys Ile Asp Thr Ile Ala Pro Asp Glu
 195 200 205

Ile Thr Val Ser Ser Asp Phe Glu Ala Arg His Val Lys Leu Asn Val
 210 215 220

Glu Glu Arg Ser Val Gly Pro Leu Thr Arg Lys Gly Phe Tyr Leu Ala
 225 230 235 240

Phe Gln Asp Ile Gly Ala Cys Val Ala Leu Leu Ser Val Arg Val Tyr
 245 250 255

Tyr Lys Lys Cys Pro Glu Leu Leu Gln Gly Leu Ala His Phe Pro Glu
 260 265 270

Thr Ile Ala Gly Ser Asp Ala Pro Ser Leu Ala Thr Val Ala Gly Thr
 275 280 285

Cys Val Asp His Ala Val Val Pro Pro Gly Gly Glu Glu Pro Arg Met
 290 295 300

His Cys Ala Val Asp Gly Glu Trp Leu Val Pro Ile Gly Gln Cys Leu
 305 310 315 320

Cys Gln Ala Gly Tyr Glu Lys Val Glu Asp Ala Cys Gln Ala Cys Ser
 325 330 335

Pro Gly Phe Phe Lys Phe Glu Ala Ser Glu Ser Pro Cys Leu Glu Cys
 340 345 350

Pro Glu His Thr Leu Pro Ser Pro Glu Gly Ala Thr Ser Cys Glu Cys
 355 360 365

Glu Glu Gly Phe Phe Arg Ala Pro Gln Asp Pro Ala Ser Met Pro Cys
 370 375 380

Thr Arg Pro Pro Ser Ala Pro His Tyr Leu Thr Ala Val Gly Met Gly
 385 390 395 400

Ala Lys Val Glu Leu Arg Trp Thr Pro Pro Gln Asp Ser Gly Gly Arg
 405 410 415

Glu Asp Ile Val Tyr Ser Val Thr Cys Glu Gln Cys Trp Pro Glu Ser
 420 425 430

Gly Glu Cys Gly Pro Cys Glu Ala Ser Val Arg Tyr Ser Glu Pro Pro
 435 440 445

His Gly Leu Thr Arg Thr Ser Val Thr Val Ser Asp Leu Glu Pro His
 450 455 460

Met Asn Tyr Thr Phe Thr Val Glu Ala Arg Asn Gly Val Ser Gly Leu
 465 470 475 480

Val Thr Ser Arg Ser Phe Arg Thr Ala Ser Val Ser Ile Asn Gln Thr
 485 490 495

Glu Pro Pro Lys Val Arg Leu Glu Gly Arg Ser Thr Thr Ser Leu Ser
 500 505 510

Val Ser Trp Ser Ile Pro Pro Pro Gln Gln Ser Arg Val Trp Lys Tyr
 515 520 525

Glu Val Thr Tyr Arg Lys Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg
 530 535 540

Arg Thr Glu Gly Phe Ser Val Thr Leu Asp Asp Leu Ala Pro Asp Thr
 545 550 555 560

Thr Tyr Leu Val Gln Val Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala
 565 570 575

Gly Ser Arg Val His Glu Phe Gln Thr Leu Ser Pro Glu Gly Ser Gly
 580 585 590

Asn Leu Ala Val Ile Gly Gly Val Ala Val Gly Val Val Leu Leu Leu
 595 600 605

Val Leu Ala Gly Val Gly Phe Phe Ile His Arg Arg Arg Lys Asn Gln
 610 615 620

Arg Ala Arg Gln Ser Pro Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln
 625 630 635 640

Leu Lys Pro Leu Lys Thr Tyr Val Asp Pro His Thr Tyr Glu Asp Pro
 645 650 655

Asn Gln Ala Val Leu Lys Phe Thr Thr Glu Ile His Pro Ser Cys Val
 660 665 670

Thr Arg Gln Lys Val Ile Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys
 675 680 685

Gly Met Leu Lys Thr Ser Ser Gly Lys Lys Glu Val Pro Val Ala Ile
 690 695 700

Lys Thr Leu Lys Ala Gly Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu
 705 710 715 720

Gly Glu Ala Gly Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg
 725 730 735

Leu Glu Gly Val Ile Ser Lys Tyr Lys Pro Met Met Ile Ile Thr Glu
 740 745 750

Tyr Met Glu Asn Gly Ala Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly
 755 760 765

Glu Phe Ser Val Leu Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala
 770 775 780

Gly Met Lys Tyr Leu Ala Asn Met Asn Tyr Val His Arg Asp Leu Ala
 785 790 795 800

Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp
 805 810 815

Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr
 820 825 830

Thr Ser Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile
 835 840 845

Ser Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Phe Gly Ile
 850 855 860

Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu
 865 870 875 880

Ser Asn His Glu Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro
 885 890 895

Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys

900 905 910
 Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe Ala Asp Ile Val Ser
 915 920 925
 Ile Leu Asp Lys Leu Ile Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala
 930 935 940
 Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser
 945 950 955 960
 Glu Gly Val Pro Phe Arg Thr Val Ser Glu Trp Leu Glu Ser Ile Lys
 965 970 975
 Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile
 980 985 990
 Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile Lys Arg Ile Gly Val
 995 1000 1005
 Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr Ser Leu Leu Gly
 1010 1015 1020
 Leu Lys Asp Gln Val Asn Thr Val Gly Ile Pro Ile
 1025 1030 1035

<210> 21
 <211> 1506
 <212> DNA
 <213> Homo sapiens

<400> 21
 cagggcaagg aagtgggtact gctggacttt gctgcagctg gaggggagct cggctggctc 60
 acacacccgt atggcaaagg gtgggacctg atgcagaaca tcatgaatga catgccgatc 120
 tacatgtact ccgtgtgcaa cgtgatgtct ggcgaccagg acaactggct ccgcaccaac 180
 tgggtgtacc gaggagaggc tgagcgtatc ttcatgagc tcaagtttac tgtacgtgac 240
 tgcaacagct tccctgggtgg cgccagctcc tgcaaggaga ctttcaacct ctactatgcc 300
 gagtcggacc tggactacgg caccaacttc cagaagcgcc tgttcaccaa gattgacacc 360
 attgcgcccg atgagatcac cgctcagcagc gacttcgagg cacgccacgt gaagctgaac 420
 gtggaggagc gctccgtggg gccgctcacc cgcaaaggct tctacctggc cttccaggat 480
 atcgggtgcct gtgtggcgct gctctccgtc cgtgtctact acaagaagtg ccccgagctg 540
 ctgcagggcc tggcccactt cctgagacc atcgccggct ctgatgcacc ttccctggcc 600

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actgtggccg gcacctgtgt ggaccatgcc gtggtgccac cgggggggtga agagccccgt    660
atgcactgtg cagtggatgg cgagtggctg gtgcccattg ggcaagtgcct gtgccaggca    720
ggctacgaga aggtggagga tgcttgccag gcctgctcgc ctggattttt taagtttgag    780
gcatctgaga gcccctgctt ggagtgcctt gagcacacgc tgccatcccc tgagggtgcc    840
acctctgcg agtgtgagga aggtttcttc cgggcacctc aggaccacgc gtcgatgcct    900
tgcacacgac cccctccgc cccacactac ctcacagccg tgggcatggg tgccaagggtg    960
gagctgcgct ggacgcccc tcaggacagc gggggcccg aggacattgt ctacagcgtc   1020
acctgcgaac agtgctggcc cgagtctggg gaatgcgggc cgtgtgaggc cagtgtgcgc   1080
tactcggagc ctctcacgg actgaccgc accagtgtga cagtgagcga cctggagccc   1140
cacatgaact acaccttcac cgtggaggcc cgcaatggcg tctcaggcct ggtaaccagc   1200
cgcagcttcc gtactgccag tgtcagcatc aaccagacag agcccccaa ggtgaggctg   1260
gagggccgca gcaccacctc gcttagcgtc tcctggagca tcccccgcc gcagcagagc   1320
cgagtgtgga agtacgaggt cacttaccgc aagaaggag actccaacag ctacaatgtg   1380
cgccgcaccg agggtttctc cgtgaccctg gacgacctgg cccagacac cacctacctg   1440
gtccagggtc aggcactgac gcaggagggc cagggggccg gcagcagggt gcacgaattc   1500
cagacg                                           1506

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<210> 22

<211> 1506

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Human sequence optimized for codon usage in *Listeria*

<400> 22

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caaggtaaag aagttgtttt attagatttt gcagcagcag gtggtgaatt aggttggtta    60
acacatccat atggtaaagg ttgggattta atgcaaaata ttatgaatga tatgccaatt   120
tatatgtata gtgtttgtaa tgttatgagt ggtgatcaag ataattgggt acgtacaaat   180
tgggtttatc gtggtgaagc agaacgtatt tttattgaat taaaatttac agttcgtgat   240
tgtaatatgt ttccagggtg tgcaagtagt tgtaaagaaa catttaattt atattatgca   300
gaaagtgatt tagattatgg taaaaatttt caaaaacgtt tatttacaaa aattgatata   360
attgcaccag atgaaattac agttagtagt gattttgaag cacgtcatgt taaattaaat   420
gttgaagaac gtagtggttg tccattaaca cgtaaagggt tttatttagc atttcaagat   480
attggtgcat gtgttgcat attaagtgtt cgtgtttatt ataaaaaatg tccagaatta   540

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ttacaagggtt tagcacattt tccagaaaca attgcaggta gtgatgcacc aagtttagca      600
acagttgcag gtacatgtgt tgatcatgca gttgttccac caggtggtga agaaccacgt      660
atgcattgtg cagttgatgg tgaatgggta gttccaattg gtcaatgttt atgtcaagca      720
ggttatgaaa aagttgaaga tgcatgtcaa gcatgtagtc caggtttttt taaatttgaa      780
gcaagtgaaa gtccatgttt agaatgtcca gaacatacat taccaagtcc agaagggtgca      840
acaagttgtg aatgtgaaga aggttttttt cgtgcaccac aagatccagc aagtatgcca      900
tgtacacgtc caccaagtgc accacattat ttaacagcag ttggtatggg tgcaaaagtt      960
gaattacggt ggacaccacc acaagatagt ggtggtcgtg aagatattgt ttatagtgtt    1020
acatgtgaac aatgttggcc agaaagtggg gaatgtggtc catgtgaagc aagtgttcgt    1080
tatagtgaac caccacatgg tttaacacgt acaagtgtta cagttagtga tttagaacca    1140
catatgaatt atacatttac agttgaagca cgtaatgggt ttagtggttt agttacaagt    1200
cgtagttttc gtacagcaag tgttagtatt aatcaaacag aaccaccaa agttcgttta    1260

gaaggtcgta gtacaacaag tttaagtgtt agttggagta ttccaccacc acaacaaagt    1320
cgtgttttga aatatgaagt tacatatcgt aaaaaagggt atagtaatag ttataatgtt    1380
cgtcgtacag aaggttttag tgttacatta gatgatttag caccagatac aacatattta    1440
gttcaagttc aagcattaac acaagaagggt caagggtgcag gtagtcgtgt tcatgaattt    1500
caaaca                                           1506

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<210> 23
 <211> 502
 <212> PRT
 <213> Homo sapeins

<400> 23

Gln Gly Lys Glu Val Val Leu Leu Asp Phe Ala Ala Ala Gly Gly Glu
 1 5 10 15

Leu Gly Trp Leu Thr His Pro Tyr Gly Lys Gly Trp Asp Leu Met Gln
 20 25 30

Asn Ile Met Asn Asp Met Pro Ile Tyr Met Tyr Ser Val Cys Asn Val
 35 40 45

Met Ser Gly Asp Gln Asp Asn Trp Leu Arg Thr Asn Trp Val Tyr Arg
 50 55 60

Gly Glu Ala Glu Arg Ile Phe Ile Glu Leu Lys Phe Thr Val Arg Asp

65					70					75				80			
Cys	Asn	Ser	Phe	Pro	Gly	Gly	Ala	Ser	Ser	Cys	Lys	Glu	Thr	Phe	Asn		
				85					90					95			
Leu	Tyr	Tyr	Ala	Glu	Ser	Asp	Leu	Asp	Tyr	Gly	Thr	Asn	Phe	Gln	Lys		
			100					105					110				
Arg	Leu	Phe	Thr	Lys	Ile	Asp	Thr	Ile	Ala	Pro	Asp	Glu	Ile	Thr	Val		
		115					120					125					
Ser	Ser	Asp	Phe	Glu	Ala	Arg	His	Val	Lys	Leu	Asn	Val	Glu	Glu	Arg		
	130					135					140						
Ser	Val	Gly	Pro	Leu	Thr	Arg	Lys	Gly	Phe	Tyr	Leu	Ala	Phe	Gln	Asp		
145					150					155					160		
Ile	Gly	Ala	Cys	Val	Ala	Leu	Leu	Ser	Val	Arg	Val	Tyr	Tyr	Lys	Lys		
				165					170					175			
Cys	Pro	Glu	Leu	Leu	Gln	Gly	Leu	Ala	His	Phe	Pro	Glu	Thr	Ile	Ala		
			180					185						190			
Gly	Ser	Asp	Ala	Pro	Ser	Leu	Ala	Thr	Val	Ala	Gly	Thr	Cys	Val	Asp		
		195					200					205					
His	Ala	Val	Val	Pro	Pro	Gly	Gly	Glu	Glu	Pro	Arg	Met	His	Cys	Ala		
	210					215					220						
Val	Asp	Gly	Glu	Trp	Leu	Val	Pro	Ile	Gly	Gln	Cys	Leu	Cys	Gln	Ala		
225					230					235					240		
Gly	Tyr	Glu	Lys	Val	Glu	Asp	Ala	Cys	Gln	Ala	Cys	Ser	Pro	Gly	Phe		
				245					250					255			
Phe	Lys	Phe	Glu	Ala	Ser	Glu	Ser	Pro	Cys	Leu	Glu	Cys	Pro	Glu	His		
			260					265					270				
Thr	Leu	Pro	Ser	Pro	Glu	Gly	Ala	Thr	Ser	Cys	Glu	Cys	Glu	Glu	Gly		
		275					280						285				
Phe	Phe	Arg	Ala	Pro	Gln	Asp	Pro	Ala	Ser	Met	Pro	Cys	Thr	Arg	Pro		
	290					295					300						
Pro	Ser	Ala	Pro	His	Tyr	Leu	Thr	Ala	Val	Gly	Met	Gly	Ala	Lys	Val		
305					310					315					320		

Glu Leu Arg Trp Thr Pro Pro Gln Asp Ser Gly Gly Arg Glu Asp Ile
 325 330 335

Val Tyr Ser Val Thr Cys Glu Gln Cys Trp Pro Glu Ser Gly Glu Cys
 340 345 350

Gly Pro Cys Glu Ala Ser Val Arg Tyr Ser Glu Pro Pro His Gly Leu
 355 360 365

Thr Arg Thr Ser Val Thr Val Ser Asp Leu Glu Pro His Met Asn Tyr
 370 375 380

Thr Phe Thr Val Glu Ala Arg Asn Gly Val Ser Gly Leu Val Thr Ser
 385 390 395 400

Arg Ser Phe Arg Thr Ala Ser Val Ser Ile Asn Gln Thr Glu Pro Pro
 405 410 415

Lys Val Arg Leu Glu Gly Arg Ser Thr Thr Ser Leu Ser Val Ser Trp
 420 425 430

Ser Ile Pro Pro Pro Gln Gln Ser Arg Val Trp Lys Tyr Glu Val Thr
 435 440 445

Tyr Arg Lys Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg Arg Thr Glu
 450 455 460

Gly Phe Ser Val Thr Leu Asp Asp Leu Ala Pro Asp Thr Thr Tyr Leu
 465 470 475 480

Val Gln Val Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala Gly Ser Arg
 485 490 495

Val His Glu Phe Gln Thr
 500

<210> 24
 <211> 1689
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion protein construct

<400> 24
 atgaaaaaaa taatgctagt ttttattaca cttatattag ttagtctacc aattgcgcaa 60

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caaactgaag caaaggatgc atctgcattc aataaagaaa attcaatttc atccatggca 120
ccaccagcat ctccgcctgc aagtcctaag acgccaatcg aaaagaaaca cgcggatctc 180
gagcagggca aggaagtggc actgctggac tttgctgcag ctggagggga gctcggctgg 240
ctcacacacc cgtatggcaa aggggtgggac ctgatgcaga acatcatgaa tgacatgccg 300
atctacatgt actccgtgtg caacgtgatg tctggcgacc aggacaactg gctccgcacc 360
aactgggtgt accgaggaga ggctgagcgt atcttcattg agctcaagtt tactgtacgt 420
gactgcaaca gcttccttgg tggcgccagc tcctgcaagg agactttcaa cctctactat 480
gccgagtcgg acctggacta cggcaccaac ttccagaagc gcctgttcac caagattgac 540
accattgcgc ccgatgagat caccgtcagc agcgacttcg aggcacgcca cgtgaagctg 600
aacgtggagg agcgcctcgt ggggcccgtc acccgcaaag gcttctacct ggccttcacg 660
gatatcgggtg cctgtgtggc gctgctctcc gtccgtgtct actacaagaa gtgccccgag 720
ctgctgcagg gcctggccca cttccctgag accatcgccg gctctgatgc accttccttg 780
gccactgtgg ccggcacctg tgtggaccat gccgtggtgc caccgggggg tgaagagccc 840
cgtatgcact gtgcagtgga tggcgagtgg ctggtgcccc ttgggcagtg cctgtgccag 900
gcaggctacg agaaggtgga ggatgcctgc caggcctgct cgctgggatt ttttaagttt 960
gaggcatctg agagcccctg cttggagtgc cctgagcaca cgctgccatc ccctgagggg 1020
gccacctcct gcgagtgtga ggaaggcttc ttccgggcac ctgaggacc agcgtcgatg 1080
ccttgcacac gacccccctc cggcccacac tacctcacag ccgtgggcat ggggtgccaa 1140
gtggagctgc gctggacgcc ccctcaggac agcggggggc gcgaggacat tgtctacagc 1200
gtcacctgcg aacagtgtgt gcccgagtct ggggaatgcg ggccgtgtga ggccagtgtg 1260
cgctactcgg agcctcctca cggactgacc cgcaccagtg tgacagtgag cgacctggag 1320
ccccacatga actacacctt caccgtggag gcccgcaatg gcgtctcagg cctggtaacc 1380
agccgcagct tccgtactgc cagtgtcagc atcaaccaga cagagcccc caaggtgagg 1440
ctggagggcc gcagcaccac ctgccttagc gtctcctgga gcatcccccc gccgcagcag 1500
agccgagtgt ggaagtacga ggtcacttac cgcaagaagg gagactccaa cagctacaat 1560
gtgcgccgca ccgaggggtt ctccgtgacc ctggacgacc tggccccaga caccacctac 1620
ctgggtccagg tgcaggcact gacgcaggag ggccaggggg ccggcagcag ggtgcacgaa 1680
ttccagacg

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<210> 25

<211> 563

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted fusion protein

<400> 25

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
 1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
 20 25 30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser
 35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Leu Glu Gln Gly Lys
 50 55 60

Glu Val Val Leu Leu Asp Phe Ala Ala Ala Gly Gly Glu Leu Gly Trp
 65 70 75 80

Leu Thr His Pro Tyr Gly Lys Gly Trp Asp Leu Met Gln Asn Ile Met
 85 90 95

Asn Asp Met Pro Ile Tyr Met Tyr Ser Val Cys Asn Val Met Ser Gly
 100 105 110

Asp Gln Asp Asn Trp Leu Arg Thr Asn Trp Val Tyr Arg Gly Glu Ala
 115 120 125

Glu Arg Ile Phe Ile Glu Leu Lys Phe Thr Val Arg Asp Cys Asn Ser
 130 135 140

Phe Pro Gly Gly Ala Ser Ser Cys Lys Glu Thr Phe Asn Leu Tyr Tyr
 145 150 155 160

Ala Glu Ser Asp Leu Asp Tyr Gly Thr Asn Phe Gln Lys Arg Leu Phe
 165 170 175

Thr Lys Ile Asp Thr Ile Ala Pro Asp Glu Ile Thr Val Ser Ser Asp
 180 185 190

Phe Glu Ala Arg His Val Lys Leu Asn Val Glu Glu Arg Ser Val Gly
 195 200 205

Pro Leu Thr Arg Lys Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly Ala
 210 215 220

Cys Val Ala Leu Leu Ser Val Arg Val Tyr Tyr Lys Lys Cys Pro Glu
 225 230 235 240

Leu Leu Gln Gly Leu Ala His Phe Pro Glu Thr Ile Ala Gly Ser Asp
 245 250 255

Ala Pro Ser Leu Ala Thr Val Ala Gly Thr Cys Val Asp His Ala Val
 260 265 270

Val Pro Pro Gly Gly Glu Glu Pro Arg Met His Cys Ala Val Asp Gly
 275 280 285

Glu Trp Leu Val Pro Ile Gly Gln Cys Leu Cys Gln Ala Gly Tyr Glu
 290 295 300

Lys Val Glu Asp Ala Cys Gln Ala Cys Ser Pro Gly Phe Phe Lys Phe
 305 310 315 320

Glu Ala Ser Glu Ser Pro Cys Leu Glu Cys Pro Glu His Thr Leu Pro
 325 330 335

Ser Pro Glu Gly Ala Thr Ser Cys Glu Cys Glu Glu Gly Phe Phe Arg
 340 345 350

Ala Pro Gln Asp Pro Ala Ser Met Pro Cys Thr Arg Pro Pro Ser Ala
 355 360 365

Pro His Tyr Leu Thr Ala Val Gly Met Gly Ala Lys Val Glu Leu Arg
 370 375 380

Trp Thr Pro Pro Gln Asp Ser Gly Gly Arg Glu Asp Ile Val Tyr Ser
 385 390 395 400

Val Thr Cys Glu Gln Cys Trp Pro Glu Ser Gly Glu Cys Gly Pro Cys
 405 410 415

Glu Ala Ser Val Arg Tyr Ser Glu Pro Pro His Gly Leu Thr Arg Thr
 420 425 430

Ser Val Thr Val Ser Asp Leu Glu Pro His Met Asn Tyr Thr Phe Thr
 435 440 445

Val Glu Ala Arg Asn Gly Val Ser Gly Leu Val Thr Ser Arg Ser Phe
 450 455 460

Arg Thr Ala Ser Val Ser Ile Asn Gln Thr Glu Pro Pro Lys Val Arg
465 470 475 480

Leu Glu Gly Arg Ser Thr Thr Ser Leu Ser Val Ser Trp Ser Ile Pro
485 490 495

Pro Pro Gln Gln Ser Arg Val Trp Lys Tyr Glu Val Thr Tyr Arg Lys
500 505 510

Lys Gly Asp Ser Asn Ser Tyr Asn Val Arg Arg Thr Glu Gly Phe Ser
515 520 525

Val Thr Leu Asp Asp Leu Ala Pro Asp Thr Thr Tyr Leu Val Gln Val
530 535 540

Gln Ala Leu Thr Gln Glu Gly Gln Gly Ala Gly Ser Arg Val His Glu
545 550 555 560

Phe Gln Thr

<210> 26
<211> 1989
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion protein construct

<400> 26
ggtacctcct ttgattagta tattcctatc ttaaagttac ttttatgtgg aggcattaac 60
atattgttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata 120
atattgcgtt tcattcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180
gtggcaaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg 240
aaaaaaataa tgctagtttt tattacactt atattagtta gtctaccaat tgcgcaacaa 300
actgaagcaa aggatgcatc tgcattcaat aaagaaaatt caatttcac ccatggcacca 360
ccagcatctc cgcttgcaag tcctaagacg ccaatcgaaa agaaacacgc ggatggatcc 420
gattataaag atgatgatga taaacaaggt aaagaagttg ttttattaga ttttgcagca 480

gcaggtggtg aattaggttg gttaacacat ccatatggta aaggttggga tttaatgcaa 540
aatattatga atgatatgcc aatttatatg tatagtgttt gtaatgttat gagggtgat 600
caagataatt gggtacgtac aaattgggtt tatcgtggtg aagcagaacg tatttttatt 660

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gaattaaaat ttacagttcg tgattgtaat agttttccag gtggtgcaag tagttgtaaa 720
gaaacattta atttatatta tgcagaaagt gatttagatt atggtacaaa ttttcaaaaa 780
cgtttattta caaaaattga tacaattgca ccagatgaaa ttacagttag tagtgatttt 840
gaagcacgtc atgttaaatt aaatgttgaa gaacgtagtg ttggtccatt aacacgtaaa 900
ggtttttatt tagcatttca agatattggg gcatgtgttg cattattaag tgttcgtggt 960
tattataaaa aatgtccaga attattacaa ggtttagcac attttccaga aacaattgca 1020
ggtagtgatg caccaagttt agcaacagtt gcaggtagat gtgttgatca tgcagttggt 1080
ccaccaggtg gtgaagaacc acgtatgcat tgtgcagttg atggtgaatg gttagttcca 1140
attgggtcaat gtttatgtca agcaggttat gaaaaagttg aagatgcatg tcaagcatgt 1200
agtccaggtt tttttaaatt tgaagcaagt gaaagtccat gtttagaatg tccagaacat 1260
acattaccaa gtccagaagg tgcaacaagt tgtgaatgtg aagaaggttt ttttcgtgca 1320
ccacaagatc cagcaagtat gccatgtaca cgtccaccaa gtgcaccaca ttatttaaca 1380
gcagttggta tgggtgcaaa agttgaatta cgttggacac caccacaaga tagtggtggt 1440
cgtgaagata ttgtttatag tgttacatgt gaacaatgtt ggccagaaag tgggtgaatgt 1500
gggccatgtg aagcaagtgt tcgttatagt gaaccaccac atggtttaac acgtacaagt 1560
gttacagtta gtgatttaga accacatatg aattatacat ttacagttga agcacgtaat 1620
gggtgtagtg gtttagttac aagtcgtagt tttcgtacag caagtgttag tattaatcaa 1680
acagaaccac caaaagttcg tttagaaggc cgtagtacia caagtttaag tgtaggttgg 1740
agtattccac caccacaaca aagtcgtggt tggaaatatg aagttacata tcgtaaaaaa 1800
ggtgatagta atagttataa tgttcgtcgt acagaagggt ttagtggtac attagatgat 1860
ttagcaccag atacaacata tttagttcaa gttcaagcat taacacaaga aggtcaagggt 1920
gcaggtagtc gtgttcatga atttcaaaca gaacaaaaat taattagtga agaagattta 1980
tgagagctc 1989

```

<210> 27

<211> 581

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted fusion protein

<400> 27

```

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
1           5           10           15

```

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
 20 25 30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser
 35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Gly Ser Asp Tyr Lys
 50 55 60

Asp Asp Asp Asp Lys Gln Gly Lys Glu Val Val Leu Leu Asp Phe Ala
 65 70 75 80

Ala Ala Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr Gly Lys Gly
 85 90 95

Trp Asp Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile Tyr Met Tyr
 100 105 110

Ser Val Cys Asn Val Met Ser Gly Asp Gln Asp Asn Trp Leu Arg Thr
 115 120 125

Asn Trp Val Tyr Arg Gly Glu Ala Glu Arg Ile Phe Ile Glu Leu Lys
 130 135 140

Phe Thr Val Arg Asp Cys Asn Ser Phe Pro Gly Gly Ala Ser Ser Cys
 145 150 155 160

Lys Glu Thr Phe Asn Leu Tyr Tyr Ala Glu Ser Asp Leu Asp Tyr Gly
 165 170 175

Thr Asn Phe Gln Lys Arg Leu Phe Thr Lys Ile Asp Thr Ile Ala Pro
 180 185 190

Asp Glu Ile Thr Val Ser Ser Asp Phe Glu Ala Arg His Val Lys Leu
 195 200 205

Asn Val Glu Glu Arg Ser Val Gly Pro Leu Thr Arg Lys Gly Phe Tyr
 210 215 220

Leu Ala Phe Gln Asp Ile Gly Ala Cys Val Ala Leu Leu Ser Val Arg
 225 230 235 240

Val Tyr Tyr Lys Lys Cys Pro Glu Leu Leu Gln Gly Leu Ala His Phe
 245 250 255

Pro Glu Thr Ile Ala Gly Ser Asp Ala Pro Ser Leu Ala Thr Val Ala
 260 265 270

Gly Thr Cys Val Asp His Ala Val Val Pro Pro Gly Gly Glu Glu Pro
 275 280 285

Arg Met His Cys Ala Val Asp Gly Glu Trp Leu Val Pro Ile Gly Gln
 290 295 300

Cys Leu Cys Gln Ala Gly Tyr Glu Lys Val Glu Asp Ala Cys Gln Ala
 305 310 315 320

Cys Ser Pro Gly Phe Phe Lys Phe Glu Ala Ser Glu Ser Pro Cys Leu
 325 330 335

Glu Cys Pro Glu His Thr Leu Pro Ser Pro Glu Gly Ala Thr Ser Cys
 340 345 350

Glu Cys Glu Glu Gly Phe Phe Arg Ala Pro Gln Asp Pro Ala Ser Met
 355 360 365

Pro Cys Thr Arg Pro Pro Ser Ala Pro His Tyr Leu Thr Ala Val Gly
 370 375 380

Met Gly Ala Lys Val Glu Leu Arg Trp Thr Pro Pro Gln Asp Ser Gly
 385 390 395 400

Gly Arg Glu Asp Ile Val Tyr Ser Val Thr Cys Glu Gln Cys Trp Pro
 405 410 415

Glu Ser Gly Glu Cys Gly Pro Cys Glu Ala Ser Val Arg Tyr Ser Glu
 420 425 430

Pro Pro His Gly Leu Thr Arg Thr Ser Val Thr Val Ser Asp Leu Glu
 435 440 445

Pro His Met Asn Tyr Thr Phe Thr Val Glu Ala Arg Asn Gly Val Ser
 450 455 460

Gly Leu Val Thr Ser Arg Ser Phe Arg Thr Ala Ser Val Ser Ile Asn
 465 470 475 480

Gln Thr Glu Pro Pro Lys Val Arg Leu Glu Gly Arg Ser Thr Thr Ser
 485 490 495

Leu Ser Val Ser Trp Ser Ile Pro Pro Pro Gln Gln Ser Arg Val Trp

500

505

510

Lys Tyr Glu Val Thr Tyr Arg Lys Lys Gly Asp Ser Asn Ser Tyr Asn
 515 520 525

Val Arg Arg Thr Glu Gly Phe Ser Val Thr Leu Asp Asp Leu Ala Pro
 530 535 540

Asp Thr Thr Tyr Leu Val Gln Val Gln Ala Leu Thr Gln Glu Gly Gln
 545 550 555 560

Gly Ala Gly Ser Arg Val His Glu Phe Gln Thr Glu Gln Lys Leu Ile
 565 570 575

Ser Glu Glu Asp Leu
 580

<210> 28
 <211> 1989
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Construct for fusion protein

<400> 28
 ggtacctcct ttgattagta tattcctatc ttaaagttac ttttatgtgg aggcattaac 60
 atttgttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata 120
 atattgcgtt tcatcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180
 gtggcaaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg 240
 aaaaaaatta tgttagtttt tattacatta attttagtta gtttaccaat tgcacaacaa 300
 acagaagcaa aagatgcaag tgcatttaat aaagaaaata gtattagtag tatggcacca 360
 ccagcaagtc caccagcaag tccaaaaaca ccaattgaaa aaaaacatgc agatggatcc 420
 gattataaag atgatgatga taaacaaggt aaagaagttg ttttattaga ttttgcagca 480
 gcaggtggtg aattaggttg gttaacacat ccatatggta aaggttggga tttaatgcaa 540
 aatattatga atgatatgcc aatttatatg tatagtgttt gtaatgttat gagtggatgat 600
 caagataatt ggttacgtac aaattgggtt tatcgtggtg aagcagaacg tattttttatt 660
 gaattaaaat ttacagttcg tgattgtaat agttttccag gtggtgcaag tagttgtaaa 720
 gaaacattta atttatatta tgcagaaaag gatttagatt atggtacaaa ttttcaaaaa 780
 cgttttattta caaaaattga tacaattgca ccagatgaaa ttacagtttag tagtgatttt 840
 gaagcacgtc atgttaaatt aaatgttgaa gaacgtagtg ttggtccatt aacacgtaaa 900

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ggtttttatt tagcatttca agatattggt gcatgtgttg cattattaag tgttcgtggt      960
tattataaaa aatgtccaga attattacaa ggtttagcac attttccaga aacaattgca    1020
ggtagtgatg caccaagttt agcaacagtt gcagggtacat gtgttgatca tgcagttggt    1080
ccaccagggtg gtgaagaacc acgtatgcat tgtgcagttg atgggtgaatg gttagttcca    1140
attgggtcaat gtttatgtca agcaggttat gaaaaagttg aagatgcatg tcaagcatgt    1200
agtccagggtt tttttaaatt tgaagcaagt gaaagtccat gtttagaatg tccagaacat    1260
acattaccaa gtccagaagg tgcaacaagt tgtgaatgtg aagaaggttt ttttcgtgca    1320
ccacaagatc cagcaagtat gccatgtaca cgtccaccaa gtgcaccaca ttatttaaca    1380
gcagttggta tgggtgcaaa agttgaatta cgttggacac caccacaaga tagtggtggt    1440
cgtgaagata ttgtttatag tgttacatgt gaacaatggt ggccagaaag tgggtgaatgt    1500
ggtccatgtg aagcaagtgt tcgttatagt gaaccaccac atggtttaac acgtacaagt    1560
gttacagtta gtgatttaga accacatatg aattatacat ttacagttga agcacgtaat    1620
ggtgttagtg gtttagttac aagtcgtagt tttcgtacag caagtgttag tattaatcaa    1680
acagaaccac caaaagttcg tttagaaggt cgtagtacaa caagtttaag tgttagttgg    1740
agtattccac caccacaaca aagtcgtggt tggaaatatg aagttacata tcgtaaaaaa    1800
ggtgatagta atagttataa tgttcgtcgt acagaagggt ttagtgttac attagatgat    1860
ttagcaccag atacaacata tttagttcaa gttcaagcat taacacaaga aggtcaagggt    1920
gcaggtagtc gtgttcatga atttcaaaca gaacaaaaat taattagtga agaagattta    1980
tgagagctc                                     1989

```

<210> 29

<211> 581

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted Fusion protein

<400> 29

```

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
1           5           10          15

```

```

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
          20          25          30

```

```

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser
35          40          45

```


Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Gly Ser Asp Tyr Lys
 50 55 60

Asp Asp Asp Asp Lys Gln Gly Lys Glu Val Val Leu Leu Asp Phe Ala
 65 70 75 80

Ala Ala Gly Gly Glu Leu Gly Trp Leu Thr His Pro Tyr Gly Lys Gly
 85 90 95

Trp Asp Leu Met Gln Asn Ile Met Asn Asp Met Pro Ile Tyr Met Tyr
 100 105 110

Ser Val Cys Asn Val Met Ser Gly Asp Gln Asp Asn Trp Leu Arg Thr
 115 120 125

Asn Trp Val Tyr Arg Gly Glu Ala Glu Arg Ile Phe Ile Glu Leu Lys
 130 135 140

Phe Thr Val Arg Asp Cys Asn Ser Phe Pro Gly Gly Ala Ser Ser Cys
 145 150 155 160

Lys Glu Thr Phe Asn Leu Tyr Tyr Ala Glu Ser Asp Leu Asp Tyr Gly
 165 170 175

Thr Asn Phe Gln Lys Arg Leu Phe Thr Lys Ile Asp Thr Ile Ala Pro
 180 185 190

Asp Glu Ile Thr Val Ser Ser Asp Phe Glu Ala Arg His Val Lys Leu
 195 200 205

Asn Val Glu Glu Arg Ser Val Gly Pro Leu Thr Arg Lys Gly Phe Tyr
 210 215 220

Leu Ala Phe Gln Asp Ile Gly Ala Cys Val Ala Leu Leu Ser Val Arg
 225 230 235 240

Val Tyr Tyr Lys Lys Cys Pro Glu Leu Leu Gln Gly Leu Ala His Phe
 245 250 255

Pro Glu Thr Ile Ala Gly Ser Asp Ala Pro Ser Leu Ala Thr Val Ala
 260 265 270

Gly Thr Cys Val Asp His Ala Val Val Pro Pro Gly Gly Glu Glu Pro
 275 280 285

Arg Met His Cys Ala Val Asp Gly Glu Trp Leu Val Pro Ile Gly Gln
 290 295 300

Cys Leu Cys Gln Ala Gly Tyr Glu Lys Val Glu Asp Ala Cys Gln Ala
 305 310 315 320

Cys Ser Pro Gly Phe Phe Lys Phe Glu Ala Ser Glu Ser Pro Cys Leu
 325 330 335

Glu Cys Pro Glu His Thr Leu Pro Ser Pro Glu Gly Ala Thr Ser Cys
 340 345 350

Glu Cys Glu Glu Gly Phe Phe Arg Ala Pro Gln Asp Pro Ala Ser Met
 355 360 365

Pro Cys Thr Arg Pro Pro Ser Ala Pro His Tyr Leu Thr Ala Val Gly
 370 375 380

Met Gly Ala Lys Val Glu Leu Arg Trp Thr Pro Pro Gln Asp Ser Gly
 385 390 395 400

Gly Arg Glu Asp Ile Val Tyr Ser Val Thr Cys Glu Gln Cys Trp Pro
 405 410 415

Glu Ser Gly Glu Cys Gly Pro Cys Glu Ala Ser Val Arg Tyr Ser Glu
 420 425 430

Pro Pro His Gly Leu Thr Arg Thr Ser Val Thr Val Ser Asp Leu Glu
 435 440 445

Pro His Met Asn Tyr Thr Phe Thr Val Glu Ala Arg Asn Gly Val Ser
 450 455 460

Gly Leu Val Thr Ser Arg Ser Phe Arg Thr Ala Ser Val Ser Ile Asn
 465 470 475 480

Gln Thr Glu Pro Pro Lys Val Arg Leu Glu Gly Arg Ser Thr Thr Ser
 485 490 495

Leu Ser Val Ser Trp Ser Ile Pro Pro Pro Gln Gln Ser Arg Val Trp
 500 505 510

Lys Tyr Glu Val Thr Tyr Arg Lys Lys Gly Asp Ser Asn Ser Tyr Asn
 515 520 525

Val Arg Arg Thr Glu Gly Phe Ser Val Thr Leu Asp Asp Leu Ala Pro
 530 535 540

Asp Thr Thr Tyr Leu Val Gln Val Gln Ala Leu Thr Gln Glu Gly Gln
 545 550 555 560

Gly Ala Gly Ser Arg Val His Glu Phe Gln Thr Glu Gln Lys Leu Ile
 565 570 575

Ser Glu Glu Asp Leu
 580

<210> 30
 <211> 1968
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion protein construct

<400> 30
 ggtacctcct ttgattagta tattcctatc ttaaagttac ttttatgtgg aggcattaac 60
 atttggttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata 120
 atattgcggtt tcatcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180
 gtggcaaacg gtatttggca ttattagggtt aaaaaatgta gaaggagagt gaaacccatg 240
 gcatacgaca gtcgttttga tgaatgggta cagaaactga aagaggaaag ctttcaaaac 300
 aatacgtttg accgcgcgaa atttattcaa ggagcgggga agattgcagg actttctctt 360
 ggattaacga ttgccagtc ggttggggcc tttggatccg attataaaga tgatgatgat 420
 aaacaaggta aagaagttgt tttattagat tttgcagcag caggtggtga attagggttg 480
 ttaacacatc catatggtaa aggttgggat ttaatgcaa atattatgaa tgatatgcca 540
 atttatatgt atagtgtttg taatgttatg agtggatgac aagataattg gttacgtaca 600
 aattgggttt atcgtggtga agcagaacgt atttttattg aattaaaatt tacagttcgt 660
 gattgtaata gttttccagg tgggtgcaagt agttgtaaag aaacatttaa tttatattat 720
 gcagaaagtg atttagatta tgggtacaaat tttcaaaaac gtttatttac aaaaattgat 780
 acaattgcac cagatgaaat tacagttagt agtgattttg aagcacgtca tggttaaatta 840
 aatggtgaag aacgtagtgt tgggtccatta acacgtaaag gtttttattt agcatttcaa 900
 gatattggtg catgtgttgc attattaagt gttcgtgttt attataaaaa atgtccagaa 960
 ttattacaag gtttagcaca ttttccagaa acaattgcag gtagtgatgc accaagttta 1020
 gcaacagttg caggtacatg tgttgatcat gcagttgttc caccaggtgg tgaagaacca 1080

```

cgtatgcatt gtgcagttga tggatgaatgg ttagttccaa ttgggtcaatg tttatgtcaa 1140
gcagggttatg aaaaagttga agatgcatgt caagcatgta gtccagggtt ttttaaattt 1200
gaagcaagtg aaagtccatg tttagaatgt ccagaacata cattaccaag tccagaaggt 1260
gcaacaagtt gtgaatgtga agaagggttt tttcgtgcac cacaagatcc agcaagtatg 1320
ccatgtacac gtccaccaag tgcaccacat tatttaacag cagttggtat ggggtgcaaaa 1380
gttgaattac gttggacacc accacaagat agtgggtggc gtgaagatat tgtttatagt 1440
gttacatgtg aacaatgttg gccagaaagt ggtgaatgtg gtccatgtga agcaagtgtt 1500
cgttatagtg aaccaccaca tggtttaaca cgtacaagtg ttacagttag tgatttagaa 1560
ccacatatga attatacatt tacagttgaa gcacgtaatg gtgtagtggtg tttagttaca 1620
agtcgtagtt ttcgtacagc aagtgttagt attaatacaa cagaaccacc aaaagttcgt 1680
ttagaagggtc gtagtacaac aagtttaagt gttagttgga gtattccacc accacaacaa 1740
agtcgtgttt ggaaatatga agttacatat cgtaaaaaag gtgatagtaa tagttataat 1800
gttcgtcgta cagaagggtt tagtgttaca ttagatgatt tagcaccaga tacaacatat 1860
ttagttcaag ttcaagcatt aacacaagaa ggtcaagggtg caggtagtcg tgttcatgaa 1920
tttcaaacag aacaaaaatt aattagttaa gaagatttat gagagctc 1968

```

<210> 31

<211> 574

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted Fusion Protein

<400> 31

```

Met Ala Tyr Asp Ser Arg Phe Asp Glu Trp Val Gln Lys Leu Lys Glu
1           5           10           15

```

```

Glu Ser Phe Gln Asn Asn Thr Phe Asp Arg Arg Lys Phe Ile Gln Gly
          20           25           30

```

```

Ala Gly Lys Ile Ala Gly Leu Ser Leu Gly Leu Thr Ile Ala Gln Ser
          35           40           45

```

```

Val Gly Ala Phe Gly Ser Asp Tyr Lys Asp Asp Asp Asp Lys Gln Gly
          50           55           60

```

```

Lys Glu Val Val Leu Leu Asp Phe Ala Ala Ala Gly Gly Glu Leu Gly
65           70           75           80

```

Trp Leu Thr His Pro Tyr Gly Lys Gly Trp Asp Leu Met Gln Asn Ile
85 90 95

Met Asn Asp Met Pro Ile Tyr Met Tyr Ser Val Cys Asn Val Met Ser
100 105 110

Gly Asp Gln Asp Asn Trp Leu Arg Thr Asn Trp Val Tyr Arg Gly Glu
115 120 125

Ala Glu Arg Ile Phe Ile Glu Leu Lys Phe Thr Val Arg Asp Cys Asn
130 135 140

Ser Phe Pro Gly Gly Ala Ser Ser Cys Lys Glu Thr Phe Asn Leu Tyr
145 150 155 160

Tyr Ala Glu Ser Asp Leu Asp Tyr Gly Thr Asn Phe Gln Lys Arg Leu
165 170 175

Phe Thr Lys Ile Asp Thr Ile Ala Pro Asp Glu Ile Thr Val Ser Ser
180 185 190

Asp Phe Glu Ala Arg His Val Lys Leu Asn Val Glu Glu Arg Ser Val
195 200 205

Gly Pro Leu Thr Arg Lys Gly Phe Tyr Leu Ala Phe Gln Asp Ile Gly
210 215 220

Ala Cys Val Ala Leu Leu Ser Val Arg Val Tyr Tyr Lys Lys Cys Pro
225 230 235 240

Glu Leu Leu Gln Gly Leu Ala His Phe Pro Glu Thr Ile Ala Gly Ser
245 250 255

Asp Ala Pro Ser Leu Ala Thr Val Ala Gly Thr Cys Val Asp His Ala
260 265 270

Val Val Pro Pro Gly Gly Glu Glu Pro Arg Met His Cys Ala Val Asp
275 280 285

Gly Glu Trp Leu Val Pro Ile Gly Gln Cys Leu Cys Gln Ala Gly Tyr
290 295 300

Glu Lys Val Glu Asp Ala Cys Gln Ala Cys Ser Pro Gly Phe Phe Lys
305 310 315 320

-38-

565

570

<210> 32
 <211> 1254
 <212> DNA
 <213> Homo sapiens

<400> 32
 caccgcagga ggaagaacca gcgtgcccgc cagtccccgg aggacgttta cttctccaag 60
 tcagaacaac tgaagcccct gaagacatac gtggaccccc acacatatga ggaccccaac 120
 caggctgtgt tgaagttcac taccgagatc catccatcct gtgtcactcg gcagaagggtg 180
 atcggagcag gagagtttgg ggagggtgtac aaggggcatgc tgaagacatc ctcggggaag 240
 aaggaggtgc cgggtggccat caagacgctg aaagccggct acacagagaa gcagcgagtg 300
 gacttcctcg gcgaggcccg catcatgggc cagttcagcc accacaacat catccgccta 360
 gagggcgctca tctccaaata caagcccatg atgatcatca ctgagtacat ggagaatggg 420
 gccctggaca agttccttcg ggagaaggat ggcgagttca gcgtgctgca gctggtgggc 480
 atgctgcggg gcatcgcagc tggcatgaag tacctggcca acatgaacta tgtgcaccgt 540
 gacctggctg cccgcaacat cctcgtcaac agcaacctgg tctgcaaggt gtctgacttt 600
 ggctgtccc gcgtgctgga ggacgacccc gagggcacct acaccaccag tggcggcaag 660
 atccccatcc gctggaccgc cccggaggcc atttcctacc ggaagttcac ctctgccagc 720
 gacgtgtgga gctttggcat tgtcatgttg gaggtgatga cctatggcga gcggccctac 780
 tgggagttgt ccaaccacga ggtgatgaaa gccatcaatg atggcttcg gctccccaca 840
 cccatggact gccctccgc catctaccag ctcatgatgc agtgctggca gcaggagcgt 900
 gcccgcgcgc ccaagttcgc tgacatcgtc agcatcctgg acaagctcat tcgtgcccct 960
 gactccctca agaccctggc tgactttgac ccccgctgt ctatccggct cccagcacg 1020
 agcggctcgg agggggtgcc cttccgcacg gtgtccgagt ggctggagtc catcaagatg 1080
 cagcagtata cggagcactt catggcggcc ggctacactg ccatcgagaa ggtggtgcag 1140
 atgaccaacg acgacatcaa gaggattggg gtgcggctgc ccggccacca gaagcgcac 1200
 gcctacagcc tgctgggact caaggaccag gtgaacactg tggggatccc catc 1254

<210> 33
 <211> 1254
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Sequence Optimized for codon usage in Listeria

<400> 33

```

cacagacgta gaaaaaatca acgtgctcga caatccccag aagatgtgta tttttcgaaa      60
agtgaacaat taaaaccatt aaaaacttat gttgatccgc atacgtacga agacccaa      120
caagcagtat taaaatttac aacagaaata cacccaagtt gtgttacaag acaaaaagtt      180
attggagcag gtgaattcgg agaggatatat aaaggatatgt taaaaacatc atcaggtaaa      240
aaagaagttc cggttgcaat taaaacctta aaggcaggat atacagaaaa acagcgagtt      300
gatttttttag gtgaagcagg aattatgggt caatttagcc atcataatat tattcgtttg      360
gaaggagtaa taagtaaata taaaccaatg atgattatta cagaatacat ggaaaacggt      420
gcttttagata aattttttacg tgaaaaggat ggtgaattta gtgttttaca attggttggt      480
atgttaagag gaattgctgc aggtatgaaa tatttagcta atatgaatta tgttcaccgt      540
gatttggcag caagaaatat cctagtcaat tccaatttag tatgtaaagt tagtgatttt      600
ggtttaagca gagtattaga agacgatcca gaggcaacct atacaacatc gggaggtaaa      660
attcctattc gttggacagc accagaagct atcagttacc gtaaatttac aagtgcac      720
gacgtgtgga gttttgggat tgtaatgtgg gaagttatga catatggaga aagaccatat      780
tgggaattaa gtaatcatga agttatgaaa gcaattaacg atggatttag attaccaact      840
ccgatggatt gtccatctgc catttatcaa ctaatgatgc aatgttggca acaagaaaga      900
gcacgacgtc caaaatttgc agatattggt agtatttttag acaaattaat tcgtgcacca      960
gatagtttaa aaacttttagc agactttgat cctcgtgtta gtattcgatt accaagtacg      1020
tcaggttccg aaggagttcc atttcgcaca gtctccgaat ggttggaatc aattaaatg      1080
caacaatata ccgaacactt tatggcagca ggttacacag caatcgaaaa agttgttcaa      1140
atgacaaaatg atgatattaa acgtattgga gttagattac caggccacca gaaacgtatt      1200
gcatattctt tattaggttt aaaagatcaa gttaataccg tgggaattcc aatt          1254

```

<210> 34

<211> 456

<212> PRT

<213> Homo sapiens

<400> 34

```

Val His Glu Phe Gln Thr Leu Ser Pro Glu Gly Ser Gly Asn Leu Ala
1              5              10              15

```

```

Val Ile Gly Gly Val Ala Val Gly Val Val Leu Leu Leu Val Leu Ala
                20              25              30

```

```

Gly Val Gly Phe Phe Ile His Arg Arg Arg Lys Asn Gln Arg Ala Arg
35              40              45

```


Gln Ser Pro Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln Leu Lys Pro
 50 55 60

Leu Lys Thr Tyr Val Asp Pro His Thr Tyr Glu Asp Pro Asn Gln Ala
 65 70 75 80

Val Leu Lys Phe Thr Thr Glu Ile His Pro Ser Cys Val Thr Arg Gln
 85 90 95

Lys Val Ile Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys Gly Met Leu
 100 105 110

Lys Thr Ser Ser Gly Lys Lys Glu Val Pro Val Ala Ile Lys Thr Leu
 115 120 125

Lys Ala Gly Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu Gly Glu Ala
 130 135 140

Gly Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg Leu Glu Gly
 145 150 155 160

Val Ile Ser Lys Tyr Lys Pro Met Met Ile Ile Thr Glu Tyr Met Glu
 165 170 175

Asn Gly Ala Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly Glu Phe Ser
 180 185 190

Val Leu Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met Lys
 195 200 205

Tyr Leu Ala Asn Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn
 210 215 220

Ile Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu
 225 230 235 240

Ser Arg Val Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr Thr Ser Gly
 245 250 255

Gly Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ser Tyr Arg
 260 265 270

Lys Phe Thr Ser Ala Ser Asp Val Trp Ser Phe Gly Ile Val Met Trp
 275 280 285

Glu Val Met Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu Ser Asn His
 290 295 300

Glu Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro Thr Pro Met
 305 310 315 320

Asp Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys Trp Gln Gln
 325 330 335

Glu Arg Ala Arg Arg Pro Lys Phe Ala Asp Ile Val Ser Ile Leu Asp
 340 345 350

Lys Leu Ile Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala Asp Phe Asp
 355 360 365

Pro Arg Val Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser Glu Gly Val
 370 375 380

Pro Phe Arg Thr Val Ser Glu Trp Leu Glu Ser Ile Lys Met Gln Gln
 385 390 395 400

Tyr Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile Glu Lys Val
 405 410 415

Val Gln Met Thr Asn Asp Asp Ile Lys Arg Ile Gly Val Arg Leu Pro
 420 425 430

Gly His Gln Lys Arg Ile Ala Tyr Ser Leu Leu Gly Leu Lys Asp Gln
 435 440 445

Val Asn Thr Val Gly Ile Pro Ile
 450 455

<210> 35

<211> 1437

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion Protein

<400> 35

atgaaaaaaa taatgctagt ttttattaca cttatattag ttagtctacc aattgcgcaa 60

caaactgaag caaaggatgc atctgcattc aataaagaaa attcaatttc atccatggca 120

ccaccagcat ctccgctgc aagtcctaag acgccaatcg aaaagaaaca cgcggatctc 180

```

gagcaccgca ggaggaagaa ccagcgtgcc cgccagtccc cggaggacgt ttacttctcc 240
aagtcagaac aactgaagcc cctgaagaca tacgtggacc cccacacata tgaggacccc 300
aaccaggctg tgttgaagtt cactaccgag atccatccat cctgtgtcac tcggcagaag 360
gtgatcggag caggagagtt tggggagggtg tacaagggca tgctgaagac atcctcgggg 420
aagaaggagg tgccggtggc catcaagacg ctgaaagccg gctacacaga gaagcagcga 480
gtggacttcc tcggcgaggc cggcatcatg ggccagtcca gccaccacaa catcatccgc 540
ctagagggcg tcatctccaa atacaagccc atgatgatca tcaactgagta catggagaat 600
ggggccctgg acaagttcct tcgggagaag gatggcgagt tcagcgtgct gcagctgggtg 660
ggcatgctgc ggggcatcgc agctggcatg aagtacctgg ccaacatgaa ctatgtgcac 720
cgtgacctgg ctgcccgcaa catcctcgtc aacagcaacc tggctctgaa ggtgtctgac 780
tttggcctgt cccgcgtgct ggaggacgac cccgaggcca cctacaccac cagtggcggc 840

aagatcccca tccgctggac cgccccggag gccatttcct accggaagtt cacctctgcc 900
agcgacgtgt ggagctttgg cattgtcatg tgggaggtga tgacctatgg cgagcggccc 960
tactgggagt tgtccaacca cgaggtgatg aaagccatca atgatggctt ccggctcccc 1020
acacccatgg actgcccctc cgccatctac cagctcatga tgcagtgtg gcagcaggag 1080
cgtgccccgc gccccaagtt cgctgacatc gtcagcatcc tggacaagct cattcgtgcc 1140
cctgactccc tcaagaccct ggctgacttt gacccccgcg tgtctatccg gctccccagc 1200
acgagcggct cggaggggggt gcccttcgc acggtgtccg agtggctgga gtccatcaag 1260
atgcagcagt atacggagca ctcatggcg gccggctaca ctgccatcga gaaggtgggtg 1320
cagatgacca acgacgacat caagaggatt ggggtgcggc tgcccggcca ccagaagcgc 1380
atcgcctaca gcctgctggg actcaaggac caggtgaaca ctgtggggat ccccatc 1437

```

<210> 36

<211> 479

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted Protein Sequence

<400> 36

```

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
1           5           10          15

```

```

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
          20          25          30

```

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser
 35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Leu Glu His Arg Arg
 50 55 60

Arg Lys Asn Gln Arg Ala Arg Gln Ser Pro Glu Asp Val Tyr Phe Ser
 65 70 75 80

Lys Ser Glu Gln Leu Lys Pro Leu Lys Thr Tyr Val Asp Pro His Thr
 85 90 95

Tyr Glu Asp Pro Asn Gln Ala Val Leu Lys Phe Thr Thr Glu Ile His
 100 105 110

Pro Ser Cys Val Thr Arg Gln Lys Val Ile Gly Ala Gly Glu Phe Gly
 115 120 125

Glu Val Tyr Lys Gly Met Leu Lys Thr Ser Ser Gly Lys Lys Glu Val
 130 135 140

Pro Val Ala Ile Lys Thr Leu Lys Ala Gly Tyr Thr Glu Lys Gln Arg
 145 150 155 160

Val Asp Phe Leu Gly Glu Ala Gly Ile Met Gly Gln Phe Ser His His
 165 170 175

Asn Ile Ile Arg Leu Glu Gly Val Ile Ser Lys Tyr Lys Pro Met Met
 180 185 190

Ile Ile Thr Glu Tyr Met Glu Asn Gly Ala Leu Asp Lys Phe Leu Arg
 195 200 205

Glu Lys Asp Gly Glu Phe Ser Val Leu Gln Leu Val Gly Met Leu Arg
 210 215 220

Gly Ile Ala Ala Gly Met Lys Tyr Leu Ala Asn Met Asn Tyr Val His
 225 230 235 240

Arg Asp Leu Ala Ala Arg Asn Ile Leu Val Asn Ser Asn Leu Val Cys
 245 250 255

Lys Val Ser Asp Phe Gly Leu Ser Arg Val Leu Glu Asp Asp Pro Glu
 260 265 270

Ala Thr Tyr Thr Thr Ser Gly Gly Lys Ile Pro Ile Arg Trp Thr Ala
 275 280 285

Pro Glu Ala Ile Ser Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val Trp
 290 295 300

Ser Phe Gly Ile Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg Pro
 305 310 315 320

Tyr Trp Glu Leu Ser Asn His Glu Val Met Lys Ala Ile Asn Asp Gly
 325 330 335

Phe Arg Leu Pro Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln Leu
 340 345 350

Met Met Gln Cys Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe Ala
 355 360 365

Asp Ile Val Ser Ile Leu Asp Lys Leu Ile Arg Ala Pro Asp Ser Leu
 370 375 380

Lys Thr Leu Ala Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro Ser
 385 390 395 400

Thr Ser Gly Ser Glu Gly Val Pro Phe Arg Thr Val Ser Glu Trp Leu
 405 410 415

Glu Ser Ile Lys Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala Gly
 420 425 430

Tyr Thr Ala Ile Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile Lys
 435 440 445

Arg Ile Gly Val Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr Ser
 450 455 460

Leu Leu Gly Leu Lys Asp Gln Val Asn Thr Val Gly Ile Pro Ile
 465 470 475

<210> 37

<211> 1737

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion protein sequence

<400> 37

ggtacctcct ttgattagta ttttcctatc ttaaagttac ttttatgtgg aggcattaac	60
at ttgttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata	120
atattgcggt tcatcttttag aagcgaat tt cgccaatatt ataattatca aaagagaggg	180
gtggcaaacg gtatttggca ttattagggt aaaaaatgta gaaggagagt gaaacccatg	240
aaaaaaataa tgctagtttt tattacactt atattagtta gtctaccaat tgcgcaacaa	300
actgaagcaa aggatgcatc tgcattcaat aaagaaaatt caatttcatc catggcacca	360
ccagcatctc cgctgcaag tctaagacg ccaatcgaaa agaaacacgc ggatggatcc	420
gattataaag atgatgatga taaacacaga cgtagaaaaa atcaacgtgc tcgacaatcc	480
ccagaagatg tgtattttttc gaaaagtga caattaaaac cattaaaaac ttatgttgat	540
ccgcatacgt acgaagacc aaatcaagca gtattaaaat ttacaacaga aatacaccca	600
agttgtgtta caagacaaaa agttattgga gcaggtgaat tcggagaggt atataaagg	660
atgttaaaaa catcatcagg taaaaaagaa gttccggttg caattaaaac cttaaaggca	720
ggatatacag aaaaacagcg agttgatttt ttaggtgaag caggaattat gggatcaatt	780
agccatcata atattattcg ttggaagga gtaataagta aatataaacc aatgatgatt	840
attacagaat acatggaaaa cggtgcttta gataaatttt tacgtgaaaa ggatggtgaa	900
tttagtgttt tacaattggg tggtatgtta agaggaattg ctgcaggtat gaaatattta	960
gctaatatga attatgttca ccgtgatttg gcagcaagaa atatcctagt caattccaat	1020
ttagtatgta aagttagtga ttttggttta agcagagtat tagaagacga tccagaggca	1080
acctatacaa catcgggagg taaaattcct attcgttgga cagcaccaga agctatcagt	1140
taccgtaaat ttacaagtgc atcagacgtg tggagttttg ggattgtaat gtgggaagtt	1200
atgacatatg gagaaagacc atattgggaa ttaagtaatc atgaagttat gaaagcaatt	1260
aacgatggat ttagattacc aactccgatg gattgtccat ctgccattta tcaactaatg	1320
atgcaatggt ggcaacaaga aagagcacga cgtccaaaat ttgcagatat tgtagtatt	1380
ttagacaaat taattcgtgc accagatagt ttaaaaaactt tagcagactt tgatcctcgt	1440
gtagtatc gattaccaag tacgtcaggt tccgaaggag ttccatttcg cacagtctcc	1500
gaatgggttg aatcaattaa aatgcaacaa tacaccgaac actttatggc agcaggttac	1560
acagcaatcg aaaaagttgt tcaaatgaca aatgatgata ttaaactgat tggagttaga	1620
ttaccaggcc accagaaacg tattgcatat tctttattag gtttaaaaga tcaagttaat	1680
accgtgggaa ttccaattga acaaaaatta atttccgaag aagacttata agagctc	1737

<210> 38

<211> 497

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted fusion protein

<400> 38

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
 1 5 10 15

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
 20 25 30

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser
 35 40 45

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Gly Ser Asp Tyr Lys
 50 55 60

Asp Asp Asp Asp Lys His Arg Arg Arg Lys Asn Gln Arg Ala Arg Gln
 65 70 75 80

Ser Pro Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln Leu Lys Pro Leu
 85 90 95

Lys Thr Tyr Val Asp Pro His Thr Tyr Glu Asp Pro Asn Gln Ala Val
 100 105 110

Leu Lys Phe Thr Thr Glu Ile His Pro Ser Cys Val Thr Arg Gln Lys
 115 120 125

Val Ile Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys Gly Met Leu Lys
 130 135 140

Thr Ser Ser Gly Lys Lys Glu Val Pro Val Ala Ile Lys Thr Leu Lys
 145 150 155 160

Ala Gly Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu Gly Glu Ala Gly
 165 170 175

Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg Leu Glu Gly Val
 180 185 190

Ile Ser Lys Tyr Lys Pro Met Met Ile Ile Thr Glu Tyr Met Glu Asn
 195 200 205

Gly Ala Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly Glu Phe Ser Val
 210 215 220

Leu Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met Lys Tyr
 225 230 235 240

Leu Ala Asn Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile
 245 250 255

Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser
 260 265 270

Arg Val Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr Thr Ser Gly Gly
 275 280 285

Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ser Tyr Arg Lys
 290 295 300

Phe Thr Ser Ala Ser Asp Val Trp Ser Phe Gly Ile Val Met Trp Glu
 305 310 315 320

Val Met Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu Ser Asn His Glu
 325 330 335

Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro Thr Pro Met Asp
 340 345 350

Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys Trp Gln Gln Glu
 355 360 365

Arg Ala Arg Arg Pro Lys Phe Ala Asp Ile Val Ser Ile Leu Asp Lys
 370 375 380

Leu Ile Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala Asp Phe Asp Pro
 385 390 395 400

Arg Val Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser Glu Gly Val Pro
 405 410 415

Phe Arg Thr Val Ser Glu Trp Leu Glu Ser Ile Lys Met Gln Gln Tyr
 420 425 430

Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile Glu Lys Val Val
 435 440 445

Gln Met Thr Asn Asp Asp Ile Lys Arg Ile Gly Val Arg Leu Pro Gly

450	455	460
His Gln Lys Arg Ile Ala Tyr Ser Leu Leu Gly Leu Lys Asp Gln Val		
465	470	475 480
Asn Thr Val Gly Ile Pro Ile Glu Gln Lys Leu Ile Ser Glu Glu Asp		
	485	490 495

Leu

<210> 39
 <211> 1737
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Fusion protein construct

<400> 39
 ggtacctcct ttgattagta tattcctatc ttaaagttac ttttatgtgg aggcattaac 60
 atttggttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata 120
 atattgcggtt tcattcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180
 gtggcaaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg 240
 aaaaaaatta tgtagttttt tattacatta atttttagtta gtttaccaat tgcacaacaa 300
 acagaagcaa aagatgcaag tgcattttaat aaagaaaata gtattagtag tatggcacca 360
 ccagcaagtc caccagcaag tccaaaaaca ccaattgaaa aaaaacatgc agatggatcc 420
 gattataaag acgatgatga taaacacaga cgtagaaaaa atcaacgtgc tcgacaatcc 480
 ccagaagatg tgtattttttc gaaaagtga caattaaaac cattaaaaac ttatgttgat 540
 ccgcatacgt acgaagaccc aaatcaagca gtattaaaat ttacaacaga aatacaccca 600
 agttgtgtta caagacaaaa agttattgga gcaggtgaat tcggagaggt atataaagg 660
 atgttaaaaa catcatcagg taaaaaagaa gttccggttg caattaaaac cttaaaggca 720
 ggatatacag aaaaacagcg agttgatttt ttaggtgaag caggaattat gggccaattt 780
 agccatcata atattattcg tttggaagga gtaataagta aatataaacc aatgatgatt 840
 attacagaat acatggaaaa cggtgcttta gataaatttt tacgtgaaaa ggatgggtgaa 900
 tttagtgttt tacaattgggt tggtatgtta agaggaattg ctgcaggtat gaaatattta 960
 gctaatatga attatgttca ccgtgatttg gcagcaagaa atatcctagt caattccaat 1020
 ttagtatgta aagttagtga ttttggttta agcagagtat tagaagacga tccagaggca 1080
 acctatacaa catcgggagg taaaattcct attcggttga cagcaccaga agctatcagt 1140

```

taccgtaaat ttacaagtgc atcagacgtg tggagttttg ggattgtaat gtgggaagtt 1200
atgacatatg gagaaagacc atattgggaa ttaagtaatc atgaagttat gaaagcaatt 1260
aacgatggat ttagattacc aactccgatg gattgtccat ctgccattta tcaactaatg 1320
atgcaatggt ggcaacaaga aagagcacga cgtccaaaat ttgcagatat tgttagtatt 1380
ttagacaaat taattcgtgc accagatagt ttaaaaactt tagcagactt tgatcctcgt 1440
gttagtattc gattaccaag tacgtcaggt tccgaaggag ttccatttcg cacagtctcc 1500
gaatggtttg aatcaattaa aatgcaacaa tacaccgaac actttatggc agcaggttac 1560
acagcaatcg aaaaagttgt tcaaatgaca aatgatgata ttaaacgtat tggagttaga 1620
ttaccaggcc accagaaacg tattgcatat tctttattag gtttaaaaga tcaagttaat 1680
accgtgggaa ttccaattga acaaaaatta atttccgaag aagacttata agagctc 1737

```

```

<210> 40
<211> 497
<212> PRT
<213> Artificial Sequence

```

```

<220>
<223> Description of Artificial Sequence: Predicted Fusion Protein

```

```

<400> 40

```

```

Met Lys Lys Ile Met Leu Val Phe Ile Thr Leu Ile Leu Val Ser Leu
1           5           10           15

```

```

Pro Ile Ala Gln Gln Thr Glu Ala Lys Asp Ala Ser Ala Phe Asn Lys
          20           25           30

```

```

Glu Asn Ser Ile Ser Ser Met Ala Pro Pro Ala Ser Pro Pro Ala Ser
          35           40           45

```

```

Pro Lys Thr Pro Ile Glu Lys Lys His Ala Asp Gly Ser Asp Tyr Lys
50           55           60

```

```

Asp Asp Asp Asp Lys His Arg Arg Arg Lys Asn Gln Arg Ala Arg Gln
65           70           75           80

```

```

Ser Pro Glu Asp Val Tyr Phe Ser Lys Ser Glu Gln Leu Lys Pro Leu
          85           90           95

```

```

Lys Thr Tyr Val Asp Pro His Thr Tyr Glu Asp Pro Asn Gln Ala Val
          100          105          110

```

```

Leu Lys Phe Thr Thr Glu Ile His Pro Ser Cys Val Thr Arg Gln Lys

```

115	120	125
Val Ile Gly Ala Gly Glu Phe Gly Glu Val Tyr Lys Gly Met Leu Lys 130 135 140		
Thr Ser Ser Gly Lys Lys Glu Val Pro Val Ala Ile Lys Thr Leu Lys 145 150 155 160		
Ala Gly Tyr Thr Glu Lys Gln Arg Val Asp Phe Leu Gly Glu Ala Gly 165 170 175		
Ile Met Gly Gln Phe Ser His His Asn Ile Ile Arg Leu Glu Gly Val 180 185 190		
Ile Ser Lys Tyr Lys Pro Met Met Ile Ile Thr Glu Tyr Met Glu Asn 195 200 205		
Gly Ala Leu Asp Lys Phe Leu Arg Glu Lys Asp Gly Glu Phe Ser Val 210 215 220		
Leu Gln Leu Val Gly Met Leu Arg Gly Ile Ala Ala Gly Met Lys Tyr 225 230 235 240		
Leu Ala Asn Met Asn Tyr Val His Arg Asp Leu Ala Ala Arg Asn Ile 245 250 255		
Leu Val Asn Ser Asn Leu Val Cys Lys Val Ser Asp Phe Gly Leu Ser 260 265 270		
Arg Val Leu Glu Asp Asp Pro Glu Ala Thr Tyr Thr Thr Ser Gly Gly 275 280 285		
Lys Ile Pro Ile Arg Trp Thr Ala Pro Glu Ala Ile Ser Tyr Arg Lys 290 295 300		
Phe Thr Ser Ala Ser Asp Val Trp Ser Phe Gly Ile Val Met Trp Glu 305 310 315 320		
Val Met Thr Tyr Gly Glu Arg Pro Tyr Trp Glu Leu Ser Asn His Glu 325 330 335		
Val Met Lys Ala Ile Asn Asp Gly Phe Arg Leu Pro Thr Pro Met Asp 340 345 350		
Cys Pro Ser Ala Ile Tyr Gln Leu Met Met Gln Cys Trp Gln Gln Glu 355 360 365		

Arg Ala Arg Arg Pro Lys Phe Ala Asp Ile Val Ser Ile Leu Asp Lys
370 375 380

Leu Ile Arg Ala Pro Asp Ser Leu Lys Thr Leu Ala Asp Phe Asp Pro
385 390 395 400

Arg Val Ser Ile Arg Leu Pro Ser Thr Ser Gly Ser Glu Gly Val Pro
405 410 415

Phe Arg Thr Val Ser Glu Trp Leu Glu Ser Ile Lys Met Gln Gln Tyr
420 425 430

Thr Glu His Phe Met Ala Ala Gly Tyr Thr Ala Ile Glu Lys Val Val
435 440 445

Gln Met Thr Asn Asp Asp Ile Lys Arg Ile Gly Val Arg Leu Pro Gly
450 455 460

His Gln Lys Arg Ile Ala Tyr Ser Leu Leu Gly Leu Lys Asp Gln Val
465 470 475 480

Asn Thr Val Gly Ile Pro Ile Glu Gln Lys Leu Ile Ser Glu Glu Asp
485 490 495

Leu

<210> 41
<211> 1716
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Fusion protein construct

<400> 41
ggtagctcct ttgattagta tattcctatc ttaaagttac ttttatgtgg aggcattaac 60
atattgttaat gacgtcaaaa ggatagcaag actagaataa agctataaag caagcatata 120
atattgcgtt tcattcttttag aagcgaattt cgccaatatt ataattatca aaagagaggg 180
gtggcaaacg gtatttggca ttattaggtt aaaaaatgta gaaggagagt gaaacccatg 240
gcatacgaca gtcgttttga tgaatgggta cagaaactga aagaggaaag ctttcaaaac 300
aatacgtttg accgccgcaa atttattcaa ggagcgggga agattgcagg actttctctt 360
ggattaacga ttgccagtc ggttggggcc tttggatccg attataaaga tgatgatgat 420

```

aaacacagac gtagaaaaaa tcaacgtgct cgacaatccc cagaagatgt gtatttttcg      480
aaaagtgaac aattaaaacc attaaaaact tatgttgatc cgcatacgta cgaagaccca      540
aatcaagcag tattaaaatt tacaacagaa atacacccaa gttgtgttac aagacaaaaa      600
gttattggag caggtgaatt cggagaggta tataaaggta tgttaaaaac atcatcaggt      660
aaaaaagaag ttccggttgc aattaaaacc ttaaaggcag gatatacaga aaaacagcga      720
gttgattttt taggtgaagc aggaattatg ggtcaattta gccatcataa tattattcgt      780
ttggaaggag taataagtaa atataaacca atgatgatta ttacagaata catggaaaac      840
ggtgctttag ataaattttt acgtgaaaag gatggtgaat ttagtgtttt acaattgggt      900
ggtatgttaa gaggaattgc tgcaggatg aaatathtag ctaatatgaa ttatgttcac      960
cgtgatttgg cagcaagaaa taccctagtc aattccaatt tagtatgtaa agttagtgat     1020
tttggtttta gcagagtatt agaagacgat ccagaggcaa cctatacaac atcggggagg      1080
aaaattccta ttcgttggac agcaccagaa gctatcagtt accgtaaatt tacaagtgca     1140
tcagacgtgt ggagttttgg gattgtaatg tgggaagtta tgacatatgg agaaagacca     1200
tattgggaat taagtaatca tgaagttatg aaagcaatta acgatggatt tagattacca     1260
actccgatgg attgtccatc tgccatttat caactaatga tgcaatgttg gcaacaagaa     1320
agagcacgac gtccaaaatt tgcagatatt gttagtattt tagacaaatt aattcgtgca     1380
ccagatagtt taaaaacttt agcagacttt gatcctcgtg ttagtattcg attaccaagt     1440
acgtcaggtt ccgaaggagt tccatttcgc acagtctccg aatggttgga atcaattaaa     1500
atgcaacaat acaccgaaca ctttatggca gcaggttaca cagcaatcga aaaagttggt     1560
caaatgacaa atgatgatat taaacgtatt ggagttagat taccaggcca ccagaaacgt     1620
attgcatatt ctttattagg tttaaaagat caagttaata ccgtgggaat tccaattgaa     1680
caaaaattaa ttccgaaga agacttataa gagctc                                  1716

```

<210> 42

<211> 490

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Predicted fusion protein

<400> 42

```

Met Ala Tyr Asp Ser Arg Phe Asp Glu Trp Val Gln Lys Leu Lys Glu
1           5           10          15

```

```

Glu Ser Phe Gln Asn Asn Thr Phe Asp Arg Arg Lys Phe Ile Gln Gly

```

20					25					30					
Ala	Gly	Lys	Ile	Ala	Gly	Leu	Ser	Leu	Gly	Leu	Thr	Ile	Ala	Gln	Ser
		35					40					45			
Val	Gly	Ala	Phe	Gly	Ser	Asp	Tyr	Lys	Asp	Asp	Asp	Lys	His	Arg	
	50					55					60				
Arg	Arg	Lys	Asn	Gln	Arg	Ala	Arg	Gln	Ser	Pro	Glu	Asp	Val	Tyr	Phe
65						70					75				80
Ser	Lys	Ser	Glu	Gln	Leu	Lys	Pro	Leu	Lys	Thr	Tyr	Val	Asp	Pro	His
				85					90					95	
Thr	Tyr	Glu	Asp	Pro	Asn	Gln	Ala	Val	Leu	Lys	Phe	Thr	Thr	Glu	Ile
			100						105					110	
His	Pro	Ser	Cys	Val	Thr	Arg	Gln	Lys	Val	Ile	Gly	Ala	Gly	Glu	Phe
			115					120					125		
Gly	Glu	Val	Tyr	Lys	Gly	Met	Leu	Lys	Thr	Ser	Ser	Gly	Lys	Lys	Glu
	130					135					140				
Val	Pro	Val	Ala	Ile	Lys	Thr	Leu	Lys	Ala	Gly	Tyr	Thr	Glu	Lys	Gln
145						150					155				160
Arg	Val	Asp	Phe	Leu	Gly	Glu	Ala	Gly	Ile	Met	Gly	Gln	Phe	Ser	His
				165					170					175	
His	Asn	Ile	Ile	Arg	Leu	Glu	Gly	Val	Ile	Ser	Lys	Tyr	Lys	Pro	Met
				180				185					190		
Met	Ile	Ile	Thr	Glu	Tyr	Met	Glu	Asn	Gly	Ala	Leu	Asp	Lys	Phe	Leu
			195				200					205			
Arg	Glu	Lys	Asp	Gly	Glu	Phe	Ser	Val	Leu	Gln	Leu	Val	Gly	Met	Leu
	210					215					220				
Arg	Gly	Ile	Ala	Ala	Gly	Met	Lys	Tyr	Leu	Ala	Asn	Met	Asn	Tyr	Val
225						230					235				240
His	Arg	Asp	Leu	Ala	Ala	Arg	Asn	Ile	Leu	Val	Asn	Ser	Asn	Leu	Val
				245					250					255	
Cys	Lys	Val	Ser	Asp	Phe	Gly	Leu	Ser	Arg	Val	Leu	Glu	Asp	Asp	Pro
			260					265					270		

Glu Ala Thr Tyr Thr Thr Ser Gly Gly Lys Ile Pro Ile Arg Trp Thr
 275 280 285

Ala Pro Glu Ala Ile Ser Tyr Arg Lys Phe Thr Ser Ala Ser Asp Val
 290 295 300

Trp Ser Phe Gly Ile Val Met Trp Glu Val Met Thr Tyr Gly Glu Arg
 305 310 315 320

Pro Tyr Trp Glu Leu Ser Asn His Glu Val Met Lys Ala Ile Asn Asp
 325 330 335

Gly Phe Arg Leu Pro Thr Pro Met Asp Cys Pro Ser Ala Ile Tyr Gln
 340 345 350

Leu Met Met Gln Cys Trp Gln Gln Glu Arg Ala Arg Arg Pro Lys Phe
 355 360 365

Ala Asp Ile Val Ser Ile Leu Asp Lys Leu Ile Arg Ala Pro Asp Ser
 370 375 380

Leu Lys Thr Leu Ala Asp Phe Asp Pro Arg Val Ser Ile Arg Leu Pro
 385 390 395 400

Ser Thr Ser Gly Ser Glu Gly Val Pro Phe Arg Thr Val Ser Glu Trp
 405 410 415

Leu Glu Ser Ile Lys Met Gln Gln Tyr Thr Glu His Phe Met Ala Ala
 420 425 430

Gly Tyr Thr Ala Ile Glu Lys Val Val Gln Met Thr Asn Asp Asp Ile
 435 440 445

Lys Arg Ile Gly Val Arg Leu Pro Gly His Gln Lys Arg Ile Ala Tyr
 450 455 460

Ser Leu Leu Gly Leu Lys Asp Gln Val Asn Thr Val Gly Ile Pro Ile
 465 470 475 480

Glu Gln Lys Leu Ile Ser Glu Glu Asp Leu
 485 490

<210> 43
 <211> 9808
 <212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion Protein Construct

<400> 43

```

ctttaaacgt ggatcatttt ctttaaattt atgctgacga cctttgaatt tgcctttttt      60
cttagcaatt tcgattcctt gtgcctgacg ttccttaatt ttttttcggt ctgattctgc      120
ttgatacttg tacaattcaa tgacaaggct attaatcaaa cgccttaaatt tttcatcttc      180
aataccattc attgagggtg aatttaagac ttccagggtt gcccccttaa tttgaatttg      240
attcatcaat tctgttaatt ctttattatt tcgtcctaatt cgatctaatt cagtaacaat      300
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 <212> PRT
 <213> *Listeria monocytogenes*

<400> 70

Thr Glu Ala Lys Asp
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<210> 71
 <211> 5
 <212> PRT
 <213> *Listeria monocytogenes*

<400> 71

Asp Lys Ala Leu Thr
 1 5

<210> 72
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 <212> PRT
 <213> *Bacillus subtilus*

<400> 72

Val Gly Ala Phe Gly
 1 5